

Result No.	Score	Query	Match	Length	DB ID	Description
1	213.5	9.1	713	1	TSA4_GITALA	P21849 giardia lam
2	202.5	8.6	3718	1	LMA5_MOUSE	Q61001 mus musculu
3	198	8.5	3084	1	LMA1_MOUSE	P19137 mus musculu
4	191	8.2	3110	1	LMA2_HUMAN	P24043 homo sapien
5	189	8.1	5376	1	ZAN_MOUSE	Q88799 mus musculu
6	187	8.0	328	1	C170_GITALA	P105799 giardia lam
7	182	7.8	657	1	TS11_GITALA	Q03185 giardia lam
8	182	7.8	3695	1	LMA5_HUMAN	Q15210 homo sapien
9	181.5	7.7	3075	1	LMA1_HUMAN	P25391 homo sapien
10	181	7.7	687	1	VS11_GITALA	P92127 giardia lam
11	178	7.6	3106	1	LMA2_MOUSE	Q60675 mus musculu
12	177.5	7.6	1607	1	LMG1_MOUSE	P02468 mus musculu
13	175	7.5	1587	1	LMG3_HUMAN	Q9y5ng homo sapien
14	173	7.4	1790	1	LMB1_DRDME	P11046 drosophila
15	172.5	7.4	1581	1	LMG3_MOUSE	Q9rb06 mus musculu
16	172	7.3	913	1	PCR5_HUMAN	Q92824 homo sapien
17	171	7.3	1576	1	YLK3_CAEEL	P41051 caenorhabdi
18	169.5	7.2	1169	1	YK82_FRAST	P36170 saccharomyces
19	169	7.2	1877	1	PCR5_MOUSE	P04592 mus musculu
20	168.5	7.2	1696	1	PKC5_BRACL	Q9n115 brachiosto
21	166.5	7.1	1557	1	LML1_CAEEL	Q18823 caenorhabdi
22	165.5	7.1	1680	1	FUR2_DRDME	P30432 drosophila
23	165.5	7.1	1700	1	BAR3_CHITE	Q03376 chironomus
24	165.5	7.1	3712	1	LMA_DRDME	Q00174 drosophila
25	162.5	6.9	2704	1	G168_PARPR	P17053 paramaecium
26	160	6.8	1609	1	LMG1_HUMAN	P11047 homo sapien
27	158.5	6.8	600	1	SP96_DICDI	P14328 dictyosteli
28	158	6.7	1246	1	YMV2_CAEEL	P34504 caenorhabdi
29	157	6.7	790	1	ANP_NOTCO	P24856 notothenia
30	156.5	6.7	2715	1	G156_PARPR	P13837 paramaecium
31	156	6.7	1192	1	LMG2_MOUSE	Q61092 mus musculu
32	154.5	6.6	1786	1	LMB1_MOUSE	P02469 mus musculu
33	154.5	6.6	2556	1	NTCL_HUMAN	P46531 homo sapien

ALIGNMENTS						
Scoring table: BLOSUM62						
Gapop 10.0 , Gapext 0.5						
Searched: 112892 seqs, 41476328 residues						
Total number of hits satisfying chosen parameters: 112892						
Minimum DB seq length: 0						
Maximum DB seq length: 2000000000						
Post-processing: Minimum Match 0%						
Maximum Match 100%						
Listing first 45 summaries						
Database : SwissProt_40:*						
RESULT 1						
TSA4_GITALA						
ID	TSA4_GITALA		STANDARD:		PRT:	713 AA.
AC	P21849;					
DT	01-MAY-1991	(Rel. 18, Created)				
DT	01-MAY-1991	(Rel. 18, Last sequence update)				
DT	16-Oct-2001	(Rel. 40, Last annotation update)				
DE	Major surface-labeled trophozoite antigen 417 precursor.					
GN	TSA 417					
OS	Giardia lamblia (Giardia intestinalis).					
OC	Eukaryota; Diplomonadida; Hexamitida; Giardinae; Giardia.					
OX	NCBI_TAXID=5741;					
[1]						
RP	SEQUENCE FROM N.A.					
RC	STRAIN=NTC 30957 / WB;					
RC	MEDLINE=90280395; PubMed=2352939;					
RA	Gillin F.D., Haggard J., Harwood J., Aley S.B., Reiner D.S.,					
RA	McCaffery M., So M., Guiney D.G.;					
RT	"Isolation and expression of the gene for a major surface protein of Giardia lamblia."					
RT	Proc. Natl. Acad. Sci. U.S.A. 87:4463-4467(1990).					
RN	[2]					
RP	SEQUENCE OF 480-620 FROM N.A.					
RC	STRAIN=AD-1;					
RC	MEDLINE=93314970; PubMed=8325510;					
RA	EY P.L., Mayrhofer G.;					
RT	"Two genes encoding homologous 70-kDa surface proteins are present within individual trophozoites of the binucleate protozoan parasite Giardia intestinalis";					
RT	Gene 129:257-262(1993).					
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ANCHORED TO THE PLASMA MEMBRANE.					
CC	-1- DOMAIN: CONTAINS 29 REPEATS OF THE CXCC MOTIF.					
CC	-1- SIMILARITY: BELONGS TO THE GIARDIA VARIANT SURFACE PROTEIN FAMILY.					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).					
CC	SMART: SM00181; EGF; 1.					
DR	M33641; AAA02688.1; -.					
DR	EMBL; M97488; AAA02581.1; -.					
DR	IN35502; A35502;					
DR	InterPro; IPR00561; EGF-like.					
DR	InterPro; IPR02174; Furin-like.					
DR	InterPro; IPR005127; Giardia_VSP.					
DR	PF03302; VSP; 2.					
DR	SMART; SM00181; EGF; 1.					
DR	SMART; SM00001; EGF; 1.					
DR	SMART; SM00261; FU; 3.					
KW	Signal; Antigen; Glycoprotein; Transmembrane; Repeat.					
FT	SIGNAL	1	17			
FT	CHAIN	18	713			



Query Match	Score	DB 1:	Length
Best Local Similarity	8.6%	Score 202.5;	3718;
Matches 94;	Conservative	Pred. No. 3.4e-06;	
		Mismatches 150;	Indels 191;
		Gaps	21;
43	TCVNCNCRPNFY-----YNGGAAQGEGANGNQPFANNAARGCIVCPQCINRVGSVTN-----91		
1842	SCQECAPIGYRTDKGLFLGICVPCOCHGHSIDRCLPGS-----GICVGQCNHTEGDCERCRPG	1899	
92	-AGDLATLATQC-STQCP-----TGALLDGVTDFVDFDR-----SAAQCYKCRPNFY	136	
1900	FVSSDESNPASPVCSCPCLAVAPSNNFADGCVLRNGRTOCLCRPGYAGASCERCAPGEF-	1958	
137	NGGSPCAEGVQFAAGAAAGYAATVQSCQCLNKKNDSPATAGAQANLIAQCSNQCP	196	
1959	--GNP-----LVISSSCQDCDSNGDPMIFEDCDPTTGACRGC-	1996	
197	TGTVLDDGVTIIVFNTSATLCKRCRPNFYNNGGSPQGEAPGVQYFAAGGAAAGVAATVSCQ	256	
1997	-----LRIHTGPCHCERCAPGFY-----	1	
257	VPCQINNKNDSPATAGAQANLIAQCSQCPSTQTAIQD-----GVTLVSNSSTQCS	306	
2023	TRC-----DCS-----PGCTETCDPQSGRCLKRGAT-----GQRCD	2054	
307	OCIANYFFNGNFEAGKSQCLKC-----PVSIETTPA-----APGNTQAOQYCL-----	350	
2055	RCLEGYF-----GFEQCCQGCRPCACGSPAAKGSECHPQSQCHCOPGTTGQCLECAPG	2107	
351	-----TICPAIGVLDGDTSTNVASETECTKCSAGF---F	382	
2108	YKLGLPEKSGCRRCQCPGRHCDPHTGHTCPGG-----LSGRDCCDSOOHQVPP	2155	
383	ASKTGFTAGTDCTECTKKL-----TSGATAKVVAEATOKVQCASTTFAK	428	

Db	2156	PGKPGHGIHCEVCDHCVVLLDGERAGLLPAIREQLQGGINASSAAWR	2206
<b>RESULT 3</b>			
	LMA1_MOUSE	STANDARD;	PT;
	ID	19137;	3084 AA.
	AC	DT 01-NOV-1990 (Rel. 16, Created)	
	DT	DT 15-JUN-2002 (Rel. 41, Last sequence update)	
	DE	Laminin alpha-1 chain precursor (Laminin A chain).	
	GN	LAMA1 OR LAMA-1 OR LAMA.	
	OS	Mus musculus (Mouse).	
	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus	
	OX	NCBI_TAXID=10090;	
	RN	[1]	
	RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	
	RX	MEDLINE=89034134; PubMed=3182802;	
	RA	Sesaki M., Kleijman H.K., Huber H., Deutzmann R., Yamada Y.;	
	RT	"Laminin, a multidomain protein. The A chain has a unique globular domain and homology with the basement membrane proteoglycan and the laminin B chains.";	
	RT	J. Biol. Chem. 263:16536-16544(1988).	
	RN	[2]	
	RP	SEQUENCE OF 1-339 FROM N.A.	
	RX	MEDLINE=88225080; PubMed=3267223;	
	RA	Hartl L., Oberbaumer I., Deutzmann R.;	
	RT	"The N terminus of Laminin A chain is homologous to the B chains.";	
	RL	Eur. J. Biochem. 173:629-635(1988)	
	RN	[3]	
	RP	SEQUENCE OF 25-38-3084 FROM N.A., AND PARTIAL SEQUENCE.	
	RX	MEDLINE=89030693; PubMed=3181157;	
	RA	Deutzmann R., Huber J., Schmetz K.A., Oberbaumer I., Hartl L.	
	RT	"Structural study of long arm fragments of laminin. Evidence for repetitive C-terminal sequences in the A-chain, not present in the B-chains.";	
	RT	Eur. J. Biochem. 177:35-45(1988).	
	RL		
	CC	-1- FUNCTION: Binding to cells via a high affinity receptor, laminin is thought to mediate the attachment, migration, and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.	
	CC	-1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three different polypeptide chains (alpha, beta, gamma), which are bound to each other by disulfide bonds into a cross-shaped molecule.	
	CC	Comprising one long and three short arms with globules at each end.	
	CC	THE ALPHA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMININ) AND LAMININ-3 (S-LAMININ).	
	CC	-1- SUBCELLULAR LOCATION: Extracellular.	
	CC	-1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR COMPONENT).	
	CC	-1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM COILED COIL STRUCTURE.	
	CC	-1- DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR.	
	CC	-1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).	
	CC	-1- SIMILARITY: CONTAINS 17 LAMININ EGF-LIKE DOMAINS.	
	CC	-1- SIMILARITY: CONTAINS 2 LAMININ G-LIKE 1.	
	CC	-1- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.	
	CC	-----	
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	CC	-----	
	DR	EMBL: J04064; AAA39410_1; -	
	DR	EMBL: X07737; CAA30561_1; -	
	DR	EMBL: X13459; CAA31807_1; -	
	DR	EMBL: M36775; AAA39406_1; -	
	DR	PIR: A31771; MMNSA.	

DR	HSSP; Q60675; 1QU0.		
DR	MGD; MGI; 99832; Lama1.		
DR	InterPro; IPR000561; EGF-like.		
DR	InterPro; IPR01886; Laminin_B.		
DR	InterPro; IPR00034; Laminin_G.		
DR	InterPro; IPR02049; Laminin_EGF.		
DR	InterPro; IPR001791; Laminin_G.		
DR	Pfam; PF00052; laminin_B; 2.		
DR	Pfam; PF00053; laminin_EGF; 15.		
DR	Pfam; PF00054; laminin_G; 5.		
DR	Pfam; PF00055; laminin_Nterm; 1.		
DR	PRINTS; PRO0011; EGFLAMININ.		
DR	PRODOM; PD002082; Laminin_1.		
DR	PRODOM; PD003031; Laminin_B; 2.		
DR	SMART; SM00180; EGF-Lam; 14.		
DR	SMART; SM00281; LamB; 2.		
DR	SMART; SM00282; LamG; 5.		
DR	SMART; SM00336; Lamin; 1.		
DR	PROSITE; PS00022; EGF_1; 11.		
DR	PROSITE; PS00025; LAM_G_DOMAIN; 5.		
DR	PROSITE; PS01186; EGF_2; 3.		
DR	PROSITE; PS01248; LAMININ_TYPE_EGF; 15.		
KW	Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil; Laminin EGF-like domain; Cell adhesion; Repeat; Signal.		
KW	LAMININ ALPHA-1 CHAIN.		
FT	SIGNAL	1	3084
FT	CHAIN	25	3084
FT	MOD_RES	25	25
FT	DOMAIN	25	25
FT	DOMAIN	25	276
FT	DOMAIN	277	333
FT	DOMAIN	334	403
FT	DOMAIN	404	460
FT	DOMAIN	461	509
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FT	DOMAIN	520	715
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FT	DOMAIN	958	1004
FT	DOMAIN	1005	1050
FT	DOMAIN	1051	1096
FT	DOMAIN	1097	1156
FT	DOMAIN	1157	1166
FT	DOMAIN	1167	1368
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FT	DOMAIN	2125	2309
FT	DOMAIN	2313	2489
FT	DOMAIN	2494	2680
FT	DISULFID	2722	2894
FT	DISULFID	2899	3079
FT	DISULFID	1612	1820
FT	DISULFID	1869	1903
FT	DISULFID	2096	2128
FT	SITE	1147	1149
FT	DISULFID	277	286
FT	DISULFID	279	297
FT	DISULFID	299	308
FT	DISULFID	311	331
FT	DISULFID	334	343
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FT	DISULFID	383	401
FT	DISULFID	404	416
FT	DISULFID	406	434
FT	DISULFID	436	445
FT	DISULFID	448	458
FT	DISULFID	461	474
FT	DISULFID	463	478

FT	DISULFID	480	489	BY SIMILARITY.	Db	810	SPTCHIUTDGFEEVVCOCAPGYSWICERADGYYGNNPTVPGG-----851	
FT	DISULFID	492	507	BY SIMILARITY.	Qy	162	AVTSQCVPCQLINKSPATAGAQANLATOCGSNQCPGTLYVENTSATLCKCRP 221	
FT	DISULFID	749	758	BY SIMILARITY.	Db	852	----TCVPCNCGNVDPLEGHCDSVTGE-----LKCLWNTDGAHCRCAD 894	
FT	DISULFID	751	764	BY SIMILARITY.	Qy	222	NFYIYGGSPQEAPGVQVFAGAAAAGV/AAVTSCQVPCQINKNDSPATAGAQANLATQCS 281	
FT	DISULFID	767	776	BY SIMILARITY.	Db	895	GFY-----GDAVTAKNCRACDCHENG-----LS 918	
FT	DISULFID	779	795	BY SIMILARITY.	Qy	282	TQCPIGTAIQDGTVLTVFNSNSSTQCSOCIANYFFNGNFRAAGSKTQPCVKPSTPAHAPGN 341	
FT	DISULFID	798	813	BY SIMILARITY.	Db	919	GVCHIUTGICLCKPKPV-----GLDTGLGCVPCNCSEGVSSVSD 968	
FT	DISULFID	800	823	BY SIMILARITY.	Qy	342	TATQATQCLTTCPAGTVLDDGTSTINFVAVSATECTKCSAGFFASKTGFTAGDTCBCTR 401	
FT	DISULFID	826	835	BY SIMILARITY.	Db	969	NCTERSQC-----HCGPQ-----VSGKQCDRCSSHGFYAFQDGG-----CPDC 1007	
FT	DISULFID	838	853	BY SIMILARITY.	Qy	402	KLTSGATAKYYAEA-----TQKVQC 421	
FT	DISULFID	856	870	BY SIMILARITY.	Db	1008	AHTQNNCDPASGECCUCPPHTQGLKC 1032	
FT	DISULFID	858	877	BY SIMILARITY.				
FT	DISULFID	880	889	BY SIMILARITY.				
FT	DISULFID	950	906	BY SIMILARITY.				
FT	DISULFID	909	921	BY SIMILARITY.				
FT	DISULFID	911	928	BY SIMILARITY.				
FT	DISULFID	930	939	BY SIMILARITY.				
FT	DISULFID	942	955	BY SIMILARITY.				
FT	DISULFID	958	970	BY SIMILARITY.				
FT	DISULFID	960	976	BY SIMILARITY.				
FT	DISULFID	978	987	BY SIMILARITY.				
FT	DISULFID	990	1002	BY SIMILARITY.				
FT	DISULFID	1005	1014	BY SIMILARITY.				
FT	DISULFID	1007	1021	BY SIMILARITY.				
FT	DISULFID	1023	1032	BY SIMILARITY.				
FT	DISULFID	1035	1048	BY SIMILARITY.				
FT	DISULFID	1051	1063	BY SIMILARITY.				
FT	DISULFID	1053	1070	BY SIMILARITY.				
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FT	DISULFID	1441	1456	BY SIMILARITY.				
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FT	DISULFID	1498	1513	BY SIMILARITY.				
FT	DISULFID	1516	1528	BY SIMILARITY.				
FT	DISULFID	1518	1535	BY SIMILARITY.				
FT	DISULFID	1537	1546	BY SIMILARITY.				
FT	DISULFID	1549	1560	BY SIMILARITY.				
FT	DISULFID	1563	1563	BY SIMILARITY.				
FT	DISULFID	1567	1567	INTERCHAIN (PROBABLE).				
FT	CARBOHYD	45	45	N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CARBOHYD	45	45	N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CARBOHYD	79	79	N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CARBOHYD	370	370	N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CARBOHYD	374	374	N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CARBOHYD	531	531	N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CARBOHYD	562	562	N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CARBOHYD	672	672	N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CARBOHYD	770	770	N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CARBOHYD	857	857	N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CARBOHYD	914	914	N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CARBOHYD	959	959	N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CARBOHYD	969	969	N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CARBOHYD	1052	1052	N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CARBOHYD	1344	1344	N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CARBOHYD	1414	1414	N-LINKED (GLCNAC. . .) (POTENTIAL).				
Query	Match	8	8.5%	Score 198; DB 1; Length 3084;				
Best Local Similarity	20.0%	Pred. No. 5.8e-06;						
Matches	89; Conservative	38; Mismatches 142; Indels 176; Gaps 16;						
Qy	23	CPG-GTQAGLTDVGADLGTCVNCRPNYYNGAAQGANGNQFAANNAARGICVPC 81						
Db	718	CPOGyN-----SEACLPGYXRVDG-----GICOPC 749						
Qy	82	QINRQGVSYTNAGDLATLQGST-----QCPTG-----						
Db	750	ECGHASECDTHGICSVYNTTGHCEQCLPGLFYTGSTPDCOPACPLSIDSNFF 809						
Qy	110	--TALDDGVTFDVR----SAAQCVKCPNFYNYGGSPQGEAPGVQWFAAGAAAAGVA 161						
Db	810	SPTCHIUTDGFEEVVCOCAPGYSWICERADGYYGNNPTVPGG-----851						
Qy	162	AVTSQCVPCQLINKSPATAGAQANLATOCGSNQCPGTLYVENTSATLCKCRP 221						
Db	852	----TCVPCNCGNVDPLEGHCDSVTGE-----LKCLWNTDGAHCRCAD 894						
Qy	222	NFYIYGGSPQEAPGVQVFAGAAAAGV/AAVTSCQVPCQINKNDSPATAGAQANLATQCS 281						
Db	895	GFY-----GDAVTAKNCRACDCHENG-----LS 918						
Qy	282	TQCPIGTAIQDGTVLTVFNSNSSTQCSOCIANYFFNGNFRAAGSKTQPCVKPSTPAHAPGN 341						
Db	919	GVCHIUTGICLCKPKPV-----GLDTGLGCVPCNCSEGVSSVSD 968						
Qy	342	TATQATQCLTTCPAGTVLDDGTSTINFVAVSATECTKCSAGFFASKTGFTAGDTCBCTR 401						
Db	969	NCTERSQC-----HCGPQ-----VSGKQCDRCSSHGFYAFQDGG-----CPDC 1007						
Qy	402	KLTSGATAKYYAEA-----TQKVQC 421						
Db	1008	AHTQNNCDPASGECCUCPPHTQGLKC 1032						
RESULT 4								
LMA2_HUMAN								
ID	LMA2_HUMAN	STANDARD;	PRN;	3110 AA.				
AC	P24043; Q14736; Q91022;							
RA	01-MAR-1992 (Rel. 21, Created)							
DT	01-MAR-1997 (Rel. 35, Last sequence update)							
RT	15-JUN-2002 (Rel. 41, Last annotation update)							
DE	Laminin alpha-2 chain precursor (Laminin M chain) (Merosin heavy chain).							
GN	LMA2 OR LAMM.							
OS	Homo sapiens (Human).							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
NCBI_TaxID	9006; RN [1]							
RP	SEQUENCE FROM N.A.							
RC	TISSUE=Placenta;							
RX	MEDLINE=94124633; PubMed=8294519;							
RA	Vuolleteaho R., Niissinen M., Sainio K., Byers M., Eddy R., Hirvonen H., Shows T.B., Sariola H., Engvall E., Tryggvason K.;							
RT	"Human laminin M chain (merosin); complete primary structure, chromosomal assignment, and expression of the M and A chain in human fibroblasts.";							
RL	J. Cell Biol. 124: 381-394 (1994).							
RN	SEQUENCE FROM 1981-3110 FROM N.A., AND PARTIAL SEQUENCE. MEDLINE=9706955; PubMed=8910357;							
RA	Zhang X., Vuolleteaho R., Tryggvason K.; "Structure of the human laminin alpha-2-chain gene (LAMA2), which is affected in congenital muscular dystrophy.";							
RT	J. Biol. Chem. 271:27664-27669 (1996).							
RL	SEQUENCE OF 1981-3110 FROM N.A., AND PARTIAL SEQUENCE. MEDLINE=90238994; PubMed=2185464;							
RA	Enrig K., Leivo I., Argraves W.S., Ruoslahti E., Engvall E.; "Merosin, a tissue-specific basement membrane protein, is a laminin-like protein"; Proc. Natl. Acad. Sci. U.S.A. 87:3264-3268 (1990).							
RT	VARIANTS GLN-545; HIS-619; LEU-919; HIS-2586 AND LYS-2614.							
RA	Panicker S.G., Mendell J.T., Chen L., Feng B., Sahlenk Z., Marzluft G.A., Amato P.A., Mendell J.R.; "Novel single base polymorphisms and rare sequence variants in the laminin 2-chain coding region detected by RNA/SSCP analysis.";							
RL	J. Biol. Chem. 271:27664-27669 (1996).							
RN	[5]							
RP	ERRATUM.							
RA	Panicker S.G., Mendell J.T., Chen L., Feng B., Sahlenk Z.,							

Marzluf G.A., Amato A.A., Mandell J.R.; *Hum. Mutat.* 13: 340-342 (1999).

-1- SUBUNIT: Laminin is a high affinity receptor, laminin is thought to mediate the attachment, migration, and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.

-1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three different polypeptide chains (alpha, beta, gamma), which are bound to each other by disulfide bonds into a cross-shaped molecule comprising one long and three short arms with globules at each end.

THE ALPHA-2 CHAIN IS A SUBUNIT OF LAMININ-2 (MEROSENIN) AND LAMININ-4 (S-MEROSIN).

-1- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT MEMBRANES (MAJOR COMPONENT).

-1- TISSUE SPECIFICITY: PLACENTA, STRIATED MUSCLE, PERIPHERAL NERVE, CARDIAC MUSCLE, PANCREAS, LUNG, SPLEEN, KIDNEY, ADRENAL GLAND, SKIN, TESTIS, MENINGES, CHOROID PLEXUS, AND SOME OTHER REGIONS OF THE BRAIN; NOT IN LIVER, THYMUS AND BONE.

-1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

-1- DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR.

-1- DISEASE: DEFECTS IN LAMA2 ARE THE CAUSE OF MEROSIN-DEFICIENT CONGENITAL MUSCULAR DYSTROPHY (CMD).

-1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).

-1- SIMILARITY: CONTAINS 17 LAMININ EGF-LIKE DOMAINS.

-1- SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.

-1- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.

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FT	DOMAIN	1166	1175	LAMININ EGF-LIKE 14 (N-TERMINAL).	RT	zonadhesin gene (ZAN).";
FT	DOMAIN	1176	1379	LAMININ DOMAIN IV 2 (DOMAIN IV A).	RL	Genomics 41:119-122(1997).
FT	DOMAIN	1380	1419	LAMININ EGF-LIKE 14 (C-TERMINAL).	CC	-1- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR SIGNALING.
FT	DOMAIN	1420	1468	LAMININ EGF-LIKE 15.	CC	-1- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
FT	DOMAIN	1469	1526	LAMININ EGF-LIKE 16.	CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE APICAL REGION OF THE SPERM HEAD.
FT	DOMAIN	1527	1573	LAMININ EGF-LIKE 17.	CC	-1- TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPLOID SPERMATIDS.
FT	DOMAIN	1574	2144	DOMAIN II AND I.	CC	-1- DOMAIN: THE MAIN DOMAINS PROBABLY MEDIATES SPERM ADHESION TO THE ZONA PELLUCIDA.
Query Match Score 8.28%; Score 191; DB 1; Length 3110;						
Best Local Similarity 24.4%; Pred. No. 1.8e-05; Mismatches 34; Gaps 30; Matches 113; Conservative 34; Domains 158; Indels 158; Gaps 30;						
Qy	42	GTCVNCR-----PNNFYNGGAQGEANGNQPFAA--NNNARGICVPCQINRVG	87		CC	-1- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS, THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF SPERMATOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS.
Db	771	GECLACKDHTGGPYCDKUCPFGY--GEPTKGTSEDCQCAPNINPSNFSPTCHDR--	826		CC	-1- DOMAIN: THE VWFED DOMAIN 2 MAY MEDIATE COVALENT OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUCIN MUC2).
Qy	88	SVTNAGDLATLATOCTSTCQPTGALDDGTVTDYDRSAAQCVRCKPNEYNGGSPQGEAPG	147		CC	-1- SIMILARITY: CONTAINS 3 MAM DOMAINS.
Db	827	-----SLGLCID-GCPVG-----	859		CC	-1- SIMILARITY: CONTAINS 25 VWF DOMAINS.
Qy	148	QVVFAGAAAAGAAYAVTSCVCPQCOLNKNDSPATAGAQANLQATQCSNQCPGTV-----	200		CC	-1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
Db	860	-----GSCQPCQCNNDLDFSPGQSDLSLSSCL-TCKPSTTGRYCELC	901		CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a licence agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
Qy	201	-----LDDGTVLVENTSATLVCVRPNFTYNGG-----SPOGEA--PGYQVFTAGAAA	246		CC	CC
Db	902	ADGYFGDAV-----DANQCPERCN--AGSFSEVCHSQTGOCERANVQGQRCDKCK	952		CC	CC
Qy	247	AGVAAVTSQL-CVPCQINKNDSPATAGAQANLQATQSCPTGTAQDGTVLVSNSSTQ	304		CC	CC
Db	953	AGTGLQSLARGCVPCNCHSFGS-----KSFDECEBSGQC----WQCPGTY-	995		CC	CC
Qy	305	CSCQIANYFENGNEAGKSQQLKCPVS-----KTPAHAPGNT-ATQATOC-----	349		CC	CC
Db	996	CDRCAHGTYF--NFOEQG--GCTACECSHLGNNCNDPPTGRCIGCKSKCAPNTWG	1050		CC	CC
Qy	350	-LTT-----CPAGTV--VASATECTKCSAGFF---ASKTTGTT	390		CC	CC
Db	1051	HSITTGCKACNACNSTVGSDLFQCNVNTGQCNCHPKFESGAKCJTECSKGHWWNPRCNJCDCFL	1110		CC	CC
Qy	391	AGTD--TTECTPKRL-----TSGATAKRYAATOKYQCASTTFF	426		CC	CC
Db	1111	PGTDAATCDSERKKCSCSDQGTCQCTKVNVEIGHCDRCRGKF	1153		CC	CC
RESULT 5						
ZAN_MOUSE	ID	ZAN_MOUSE	STANDARD:	PRT;	5376 AA.	
AC	O87799; Q08647;					
DT	16-OCT-2001 (Rel. 40, Created)					
DT	16-OCT-2001 (Rel. 40, Last sequence update)					
DT	16-OCT-2001 (Rel. 40, Last annotation update)					
DE	Zonadhesin precursor.					
GN	ZAN.					
OS	Mus musculus (Mouse).					
OC	Eukaryota; Metazoa; Chordata; Crustacea; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OX	NCBI_TaxID=10090;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Testis;					
RX	MEDLINE=98123114; PubMed=9452463;					
RA	Gao Z., Garbers D.L.;					
RT	"Species diversity in the structure of zonadhesin, a sperm-specific membrane protein containing multiple cell adhesion molecule-like domains."					
RL	J. Biol. Chem. 273:3415-3421(1998).					
RN	[2]					
RC	SEQUENCE OF 4864-5376 FROM N.A.					
RC	TISSUE=Testis;					
RX	MEDLINE=9727156; PubMed=9126492;					
RA	Gao Z., Harumi T., Garbers D.L.;					
RT	"Chromosome localization of the mouse zonadhesin gene and the human					
RT	RT	RT	RT	RT	POTENTIAL.	
RT	RT	RT	RT	RT	ZONADHESIN.	
RT	RT	RT	RT	RT	EXTRACELLULAR (POTENTIAL).	
RT	RT	RT	RT	RT	POTENTIAL.	
RT	RT	RT	RT	RT	CYTOSMERIC (POTENTIAL).	
RT	RT	RT	RT	RT	POTENTIAL.	
RT	RT	RT	RT	RT	80 X HEPTAPEPTIDE REPEATS (APPROXIMATE)	
RT	RT	RT	RT	RT	(MUCIN-LIKE DOMAIN).	
RT	RT	RT	RT	RT	VWF 1 (PARTIAL).	
RT	RT	RT	RT	RT	VWF 2 (PARTIAL).	
RT	RT	RT	RT	RT	VWF 3.	
RT	RT	RT	RT	RT	VWF 4.	
RT	RT	RT	RT	RT	VWF 5 (PARTIAL).	
RT	RT	RT	RT	RT	VWF 6 (PARTIAL).	
RT	RT	RT	RT	RT	VWF 7 (PARTIAL).	
RT	RT	RT	RT	RT	VWF 8 (PARTIAL).	
RT	RT	RT	RT	RT	VWF 9 (PARTIAL).	
RT	RT	RT	RT	RT	VWF 10 (PARTIAL).	



Qy 135 YYNGGSPQGEAPGVYFAAGAAAAGVAAVTISQCVPCQLN-----KNDSPATAGAQANLA 188  
 Db 104 -----APTCAGTA-----DKC1KCDANGAAPYLKKTNPSPDPTGTCVYSA 143  
 Qy 189 TQCSNOCPTGTVLDDGVTVNTSATLCKCRPNFYNGSPQEBAPGVQEAGAAAAG 248  
 Db 144 VDC----QGSAKYTDDSV----SDAKECKRC-----AEQKPN-----TAG 177  
 Qy 249 VAAVTISQCVPCQINNDSPATAGAOANLTCST-----AQPTGT-----AQDGYT-L 296  
 Db 178 ----TQFSC----SDANCERCQDQGARCSNGAPPNGKCPAATDQCHSSCDGCTEN 228  
 Qy 297 VFSNNSTQCQSQCANYFFNGNFEEKS-----KCPVSKTTPAHPGNATQATOCLT 352  
 Db 229 AMTNGADKCTGCKGCKEGRYLPESSAQNQSGCLTAECTSDKT----HFTREKAGDSKGmLS 285  
 Qy 353 CPAGTVLDDGTSTNFVASATECTKCSAGFFASKT-TGFTAGTDTCTECT-KKLTSGATA 409  
 Db 286 CSDAT-----HGTTGCKC-----ALKTLSGEAESTVVCSECTDKRLLTSPGNA 328

## RESULT 7

TS11\_GIALA  
 ID TS11\_GIALA STANDARD; PRT; 667 AA.  
 AC Q03185;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 15-JUL-1994 (Rel. 29, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Major surface trophozoite antigen 11 precursor.  
 GN TSP1.  
 OS Giardia lamblia (Giardia intestinalis).  
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.  
 OX NCBI\_TAXID=5741;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=332411215; PubMed=8479449;  
 RA EY P.L., Khanna K., Manning P.A., Mayrhofer G.;  
 RT A gene encoding a 69-kilodalton major surface protein of Giardia  
 intestinalis trophozoites.  
 RL Mol. Biochem. Parasitol. 58:247-258(1993).  
 CC SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ANCHORED TO THE  
 CC PLASMA MEMBRANE.  
 CC DOMAIN: CONTAINS 27 REPEATS OF A CXXC MOTIF.  
 CC - SIMILARITY: BELONGS TO THE GIARDIA VARIANT SURFACE PROTEIN FAMILY.

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 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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 CC entities requires a license agreement (See <http://www.1sb-sib.ch/announce/>  
 CC or send an email to license@1sb-sib.ch).  
 DR EMBL; M95814; AAA02687.1; -.  
 DR PIR; A48579; A48579.  
 DR HSSP; P02468; 1KLO.  
 DR InterPro; IPR00561; EGF-like.  
 DR InterPro; IPR002174; Furin-like.  
 DR InterPro; IPR005127; Giardia\_VSP.  
 DR Pfam; PF03302; VSP; 1.  
 DR SMART; SM00181; EGF; 3.  
 DR SMART; SM00261; FU; 5.  
 KW Antigen; Repeat; Transmembrane; Signal.  
 FT DOMAIN 1 17 MAJOR SURFACE TROPHOZOITE ANTIGEN 11.  
 FT DOMAIN 1 18 667 MAJOR SURFACE TROPHOZOITE ANTIGEN 11.  
 FT DOMAIN 1 18 633 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 634 662 CITOPLASMIC (POTENTIAL).  
 FT DOMAIN 663 667 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 591 591 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 630 630 68475 MW; 1DD957270323BBD CRC64;

Query Match 7.8%; Score 182; DB 1; Length 667;  
 Best Local Similarity 22.2%; Pred. No. 1; e-05;  
 Matches 120; Conservative 42; Mismatches 170; Indels 208; Gaps 32;  
 Qy 7 LILIIISLFINELRAVPCPDGTQ-----QAGLTDY-----GAADL-GTCVNCRPNFY 52  
 Db 1 MLLAIFYEVISTLATACTTQTCATCEARCEMYGETCTRCGKPVDFGRGVCDATAN-- 58  
 Qy 53 YNGGAQGEANGNQPFQAAANAAARG--ICVPCQINRGSVT-----NAGDLATLATQC 102  
 Db 59 ANCKNASEDGDANQVCGRMSSVPGNTLCTTVSPDGCSVAANEYFVPPNADATHDSVVSC 118  
 Qy 103 SPTQCPGTALDDGVTDYFDRSAQCTYKCKPFPFYNGSPQCBAPGVQFARGAAAGVAA 162  
 Db 119 SPTEPHILANKQYIGV-----AGCATC-----SAP-----KAPGDNTPKAAT----- 157  
 Qy 163 VTSQCVPCQLNKNDSPTAGAQANLTCQTSNQCTQPTVLDGVTLVFNTSAT-----LCV 217  
 Db 158 ---CTPKCAAGFLHTPSEG-----LSSCETCPSEG-----YFGHTATAESKTKCK 198  
 Qy 218 KCRPNFYYNGSPQGEAPGVYFAAGAAAAGVAAVTSQCVPCQINRNDSPATAGAQANLA 277  
 Db 199 SC-----TGGS-----SEAPNVK-----ASGNLT 229  
 Qy 278 T--QCSTQ-----CPTGTA1QDGTVLVSNSITQ- 304  
 Db 230 TCEBKCSAQKPKSLDKTNSCNDTGQNCNAFCSSSGGDCEGCDSG-F1D1GQNCVKSQCDKT 288  
 Qy 305 -----SCSOCIANYFFN-----GNFEG-----KSQCLKCPVS--K 332  
 Db 289 CKACTNPKAAANEVCTCISIHLHTPSQCVQYQCAQALGNYYAGTNADNKKACKECTVANCK 348  
 Qy 333 T-----TPHAHPGNT-----ATQATOCLTTECPATVY-----DDG1STN 366  
 Db 349 TCNDQGOCQTNDGFYKNGDAGCSPHESCKTCISAGTASDC-TECPGKALKYGNNDTK-- 405  
 Qy 367 FVASATEPCTKCSAGFFASKT-----GTDTCETCEPKLTKLTSGATAKYAATQKVOCASST 425  
 Db 406 -GTCCGGCTGTQGSSGACKTGLTIDGASYCSECDTQ-----NEYPONGICSTT 453

## RESULT 8

IMA5\_HUMAN  
 ID IMA5\_HUMAN STANDARD; PRT; 3695 AA.  
 AC Q15230; Q9H1P1; Q8WZA7;  
 DR 16-OCT-2001 (Rel. 40, Created)  
 DR 15-JUN-2002 (Rel. 41, Last sequence update)  
 DR 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE LAMINA5 OR KIAA0533 OR KIAA1907.  
 GN Homo sapiens (Human).  
 OS Homo sapiens (Human).  
 OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TAXID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 ID IMA5\_HUMAN STANDARD;  
 AC Q15230; Q9H1P1; Q8WZA7;  
 DR 16-OCT-2001 (Rel. 40, Created)  
 DR 15-JUN-2002 (Rel. 41, Last sequence update)  
 DR 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE LAMINA5 OR KIAA0533 OR KIAA1907.  
 RN MEDLINE=21638749; PubMed=11780052;  
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavridis G., Almeida J.P., Babage C.K., Bagguley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blailey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carter C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Connor R.E., Clegg S.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French J., Garner P.,  
 RA Graham D.V., Griffiths M.N.D., Guillen R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Key M.P., Kimerer A.M., King G.K., Laird A.J., Lovell J.D., Lovell J.D.,  
 RA Lehyaslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,



FT	DISULFID	408	426	BY SIMILARITY.
FT	DISULFID	429	440	BY SIMILARITY.
FT	DISULFID	431	447	BY SIMILARITY.
FT	DISULFID	449	458	BY SIMILARITY.
FT	DISULFID	461	471	BY SIMILARITY.
FT	DISULFID	494	506	BY SIMILARITY.
FT	DISULFID	496	515	BY SIMILARITY.
FT	DISULFID	517	526	BY SIMILARITY.
FT	DISULFID	529	538	BY SIMILARITY.
FT	DISULFID	541	553	BY SIMILARITY.
FT	DISULFID	543	560	BY SIMILARITY.
FT	DISULFID	562	571	BY SIMILARITY.
FT	DISULFID	574	584	BY SIMILARITY.
FT	DISULFID	587	599	BY SIMILARITY.
FT	DISULFID	599	605	BY SIMILARITY.
FT	DISULFID	607	616	BY SIMILARITY.
FT	DISULFID	619	629	BY SIMILARITY.
FT	DISULFID	632	644	BY SIMILARITY.
FT	DISULFID	634	650	BY SIMILARITY.
FT	DISULFID	652	661	BY SIMILARITY.
FT	DISULFID	664	674	BY SIMILARITY.
FT	DISULFID	677	689	BY SIMILARITY.
FT	DISULFID	679	696	BY SIMILARITY.
FT	DISULFID	698	707	BY SIMILARITY.
FT	DISULFID	710	720	BY SIMILARITY.
Query Match		7.8%	Score 182; DB 1; Length 3695;	
Best Local Similarity	21.8%	Pred. No. 8.5e-05;		
Matches	97;	Conservative 38; Mismatches 171; Indels 138; Gaps 25;		
Qy	43	TCVNCRPNFY-----YNGGAAQGEANGNQPFAAANNARGICVCPQCIN-----RVG 87		
Db	1841	SCOECAFGYPRDKVKGFLGRCPQCHGSDRCLPGS-->GCVYDQCHNTEGARGERCQAG 1898		
Qy	88	SYVNAGGDLATLATOCSQCP-----TGTALDDGVIDVDFDRSAACQVCKCPNPFYNG 138		
Db	1899	FVSSRDPDSPAPCVSC-->PCPUSVPSINFAQGCVLRGGRT-----QCLL-CRPG--TAG 1945		
Qy	139	GSPQGERAPGVQYFAAGAAAAGVAAATSQSCVCPQCLNKNDSPATAGAQANATCQSNQCTG 198		
Db	1946	ASCERAPG-->FFGNPLVLG-----SCQCPDCSGNGPNNLFSDCDPLTGCRGC--- 1994		
Qy	199	TVLDDGTVLVTNTSATLCKVCRPNFYNGGSPQGEAPGVQYFAAGAAAAG-----VA 250		
Db	1995	-----LRTHTGPRCEICAPYGNVNLPLP-GNCTRDCTPGTEADPHSGHCLKA 2044		
Qy	251	AVTSQ-----CVPQIQINKNDSPATAGAQAN-LATCQSTCOPGTGTAQD 292		
Db	2045	GVTGRRCDRQEGHFGNGGGRCAC-->GAAEGSECHQSGQG--HCRPGT---- 2094		
Qy	293	GVTLYFNSNSTQSCSCLANYFFGNFNEAGKPSKTTPAHAPNTAQATQCLTT 352		
Db	2095	-----MGPQCRCRAPGWW--GLPDEGCRRC-QCPCGRCDP-----HTGRC--N 2132		
Qy	353	CPAGTVLDDGSTNTFVAASATECTMCAGF-->PASKRTGFTACTDTCTCCTCTKRL---T 404		
Db	2133	CPPG-----LGERCDTCQSQHQVQPVGGPVGHSIHCEVCDHVYLLDDLER 2180		
Qy	405	SGATKAYAETOKVQCASTTFK 428		
Db	2181	AGALLPAIHEQLRQJNASSMAWAR 2204		
RESULT	9			
ID	LMA1_HUMAN	STANDARD;	PRP;	3075 AA.
AC	P23931;			
DT	01-MAY-1992	(Rel. 22, Created)		
DT	01-MAY-1993	(Rel. 22, last sequence update)		
DT	15-JUN-2002	(Rel. 41, last annotation update)		
DE	Laminin alpha-1 chain precursor (Laminin A chain)			
GN	LAMA1 OR LAMA1			
DR	Homo sapiens (Human).			

PRODOM;	PD003031;	Laminin_B;	2.
SMART;	SM00180;	EGF_Lam;	14.
SMART;	SM00001;	EGF-like;	1.
SMART;	SM00281;	LamB;	2.
SMART;	SM00282;	LamG;	5.
SMART;	SM00136;	LamNT;	1.
PROSITE;	PS00022;	EGF_1;	11.
PROSITE;	PS01186;	EGF_2;	2.
PROSITE;	PS01248;	LAMININ_TYPE_EGF;	15.
PROSITE;	PS50025;	LAM_G_DOMAIN;	5.
Glycoprotein; Basement_matrix; Extracellular_matrix; Coiled_coil;			
Laminin EGF-like domain; Cell adhesion; Repeat; Signal.			
SIGNAL	1	POTENTIAL.	
CHAIN	18	3075	LAMININ_ALPHA-1 CHAIN.
DOMAIN	18	269	LAMININ_N-TERMINAL (DOMAIN VI).
DOMAIN	270	326	LAMININ_EGF-LIKE 1.
DOMAIN	327	396	LAMININ_EGF-LIKE 2.
DOMAIN	397	453	LAMININ_EGF-LIKE 3.
DOMAIN	454	502	LAMININ_EGF-LIKE 4.
DOMAIN	503	512	LAMININ_EGF-LIKE 5 (N-TERMINAL).
DOMAIN	517	708	LAMININ_DOMAIN_IV_1 (DOMAIN IV_B).
DOMAIN	709	741	LAMININ_EGF-LIKE 5 (C-TERMINAL).
DOMAIN	742	790	LAMININ_EGF-LIKE 6.
DOMAIN	791	848	LAMININ_EGF-LIKE 7.
DOMAIN	849	901	LAMININ_EGF-LIKE 8.
DOMAIN	902	950	LAMININ_EGF-LIKE 9.
DOMAIN	951	997	LAMININ_EGF-LIKE 10.
DOMAIN	998	1043	LAMININ_EGF-LIKE 11.
DOMAIN	1044	1089	LAMININ_EGF-LIKE 12.
DOMAIN	1080	1149	LAMININ_EGF-LIKE 13.
DOMAIN	1150	1159	LAMININ_EGF-LIKE 14 (N-TERMINAL).
DOMAIN	1160	1361	LAMININ_DOMAIN_IV_2 (DOMAIN IV_A).
DOMAIN	1362	1402	LAMININ_EGF-LIKE 14 (C-TERMINAL).
DOMAIN	1403	1451	LAMININ_EGF-LIKE 15.
DOMAIN	1452	1508	LAMININ_EGF-LIKE 16.
DOMAIN	1509	1555	LAMININ_EGF-LIKE 17.
DOMAIN	1556	2116	DOMAIN_II_AND_I.
DOMAIN	2117	2297	LAMININ_G-LIKE 1.
DOMAIN	2305	2481	LAMININ_G-LIKE 2.
DOMAIN	2486	2673	LAMININ_G-LIKE 3.
DOMAIN	2713	2885	LAMININ_G-LIKE 4.
DOMAIN	2890	3070	LAMININ_G-LIKE 5.
DOMAIN	1706	1796	COILED_COIL (POTENTIAL).
DOMAIN	1968	1989	COILED_COIL (POTENTIAL).
DOMAIN	2088	2120	COILED_COIL (POTENTIAL).
SITE	2534	2536	CELL_ATTACHMENT_SITE.
DISULFID	270	279	BY SIMILARITY.
DISULFID	272	290	BY SIMILARITY.
DISULFID	292	301	BY SIMILARITY.
DISULFID	297	305	POTENTIAL.
DISULFID	304	324	BY SIMILARITY.
DISULFID	327	336	BY SIMILARITY.
DISULFID	329	361	BY SIMILARITY.
DISULFID	364	373	BY SIMILARITY.
DISULFID	376	394	BY SIMILARITY.
DISULFID	397	409	BY SIMILARITY.
DISULFID	427	427	BY SIMILARITY.
DISULFID	429	438	BY SIMILARITY.
DISULFID	441	451	BY SIMILARITY.
DISULFID	454	467	BY SIMILARITY.
DISULFID	456	471	BY SIMILARITY.
DISULFID	473	482	BY SIMILARITY.
DISULFID	485	500	BY SIMILARITY.
DISULFID	742	751	BY SIMILARITY.
DISULFID	744	757	BY SIMILARITY.
DISULFID	760	769	BY SIMILARITY.
DISULFID	762	788	BY SIMILARITY.
DISULFID	791	806	BY SIMILARITY.
DISULFID	793	816	BY SIMILARITY.
DISULFID	819	828	BY SIMILARITY.
DISULFID	831	846	BY SIMILARITY.
DISULFID	849	863	BY SIMILARITY.
DISULFID	851	870	BY SIMILARITY.

Db	72	DGTALDKTAT-----TCGKCGDGYFLFMGGCYKTE---SOPGSEICITTAASNLGCTAC	120
Qy	82	QINRVSSTVNAGDIALTATOCSTOCTPTGTAIDDGTVDFDRS---AAQCYVKCPNPFYNN	137
Db	121	KYDSQYIFQNKATPPEKGSCSIL-----CWDPTDRGVMGANCAT-----	162
Qy	138	GSPQGEAPGVQVFAARGAAAAGVVAAT-----SOCVPCOLNKNDSPATAGAQAN	186
Db	163	-----TAPASSTGPATCTECMAGTYKKSDTEAACAH-----SDCATSCSEANN	205
Qy	187	LATQC-----SNO-----CPGTVDGGTVLWVFTNTSATL---CV	217
Db	206	QCTSCETGTKYLKSRQCVENCTCNTHYPDDTSMTVCVACTVLDANCATCSFSDSATKGKCL	265
Qy	218	KCRPNFYYNGGSPQ---GEAPGVQVFAAGAAA-----	247
Db	266	TCNSN-----KIPPTFLDGTSTCAGTENSAGCQAGDNLEFMKDQSAQCLLGDTRKASNDK	320
Qy	248	GVAATISQCVPCQ1NKNDSPATAGA-----QANILATOCSTOCPTGTATQDGTVLTVFS	299
Db	321	GVA---NCRTCTNANDNSPPCTACLDGYFELRGSCSTTCAADNATCSE-----A	367
Qy	300	NSSTOCSOCTANYFENGNEFAGKSQCLKCPVSKTTPAHAPGNTATAQTLTTCAGTIVL	359
Db	368	TTEDECKICKAGFPL---ASPGIGKCIISC---SDTNNGGIDG---CAEC-TKEPAGPL-	415
Qy	360	DDGTSNTNFVASATETCTKOSAGFPASSKTFGTAGTDCCTEYKKL-----TSGATAK	410
Db	416	-----KTCRKC-----KPNRKPAAGTSNDNTCTEKTCEDPTIVCGGTSGACDR	455
Qy	411	VYEAQTQK 418	
Db	456	IVIDANGK 463	
RESULT 11			
LMA2_MOUSE			
ID	LMA2_MOUSE	STANDARD	PRT;
AC	060575;	Q05003; Q64061;	
DT	01-NOV-1997	(Rel. 35, Created)	
DT	01-NOV-1997	(Rel. 35, Last sequence update)	
DT	15-JUN-2002	(Rel. 41, Last annotation update)	
DE	Laminin alpha-2 chain precursor	(Laminin M chain)	(Merosin heavy chain).
DE	LAMA2.		
GN	Mus musculus (Mouse).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX			
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN="FB/N"; TISSUE="Embryo, and Heart;		
RX	MEDLINE=95316259; PubMed=795883;		
RA	Bernier S.M., Utani A., Sugiyama S., Doi T., Polistina C.,		
RA	Yanada Y.		
RT	"Cloning and expression of laminin alpha 2 chain (M-chain) in the		
RT	mouse."		
RL	Matrix Biol. 14: 447-455(1995).		
RN	[2]		
RP	SEQUENCE OF 2162-2279 FROM N.A.		
RC	STRAIN="C57BL/6"; TISSUE="Thymus,"		
RX	MEDLINE=93346725; PubMed=8345183;		
RA	Chang A.C., Wadsworth S., Coligan J.E.;		
RT	"Expression of meroisin in the thymus and its interaction with		
RT	thymocytes."		
RN	J. Immunol. 151: 1789-1801(1993).		
RP	SEQUENCE OF 64-281 FROM N.A.		
RC	MEDLINE=95179178; PubMed=7874173;		
RA	Xu H., Wu X.R., Wever U.M., Engvall E.;		
RT	"Murine muscular dystrophy caused by a mutation in the laminin alpha 2 (Lama2) gene."		
RT	Nat. Genet. 8: 297-302(1994).		

TT	410	464	LAMININ EGF-LIKE 3.
DOMAIN	465	523	LAMININ EGF-LIKE 4.
DOMAIN	514	523	LAMININ EGF-LIKE 5 (N-TERMINAL).
DOMAIN	524	719	LAMININ DOMAIN IV 1 (DOMAIN IV B).
DOMAIN	720	752	LAMININ EGF-LIKE 5 (C-TERMINAL).
DOMAIN	753	802	LAMININ EGF-LIKE 6.
DOMAIN	803	860	LAMININ EGF-LIKE 7.
DOMAIN	861	913	LAMININ EGF-LIKE 8.
DOMAIN	914	962	LAMININ EGF-LIKE 9.
DOMAIN	963	1009	LAMININ EGF-LIKE 10.
DOMAIN	1010	1055	LAMININ EGF-LIKE 11.
DOMAIN	1056	1101	LAMININ EGF-LIKE 12.
DOMAIN	1102	1161	LAMININ EGF-LIKE 13.
DOMAIN	1162	1171	LAMININ EGF-LIKE 14 (N-TERMINAL).
DOMAIN	1172	1375	LAMININ DOMAIN IV 2 (DOMAIN IV A).
DOMAIN	1376	1415	LAMININ EGF-LIKE 14 (C-TERMINAL).
DOMAIN	1416	1464	LAMININ EGF-LIKE 15.
DOMAIN	1465	1522	LAMININ EGF-LIKE 16.
DOMAIN	1523	1569	LAMININ EGF-LIKE 17.
DOMAIN	1574	2140	DOMAIN II AND I.
DOMAIN	2141	2324	LAMININ G-LIKE 1.
DOMAIN	2336	2517	LAMININ G-LIKE 2.
DOMAIN	2522	2706	LAMININ G-LIKE 3.
DOMAIN	2759	2930	LAMININ G-LIKE 4.
DOMAIN	2929	3106	LAMININ G-LIKE 5.
DOMAIN	3162	3186	COILED COIL (POTENTIAL).
DOMAIN	1923	2146	COILED COIL (POTENTIAL).
DISULFID	283	292	BY SIMILARITY.
DISULFID	285	303	BY SIMILARITY.
DISULFID	305	314	BY SIMILARITY.
DISULFID	317	337	BY SIMILARITY.
DISULFID	340	349	BY SIMILARITY.
DISULFID	342	374	BY SIMILARITY.
DISULFID	377	386	BY SIMILARITY.
DISULFID	389	407	BY SIMILARITY.
DISULFID	410	422	BY SIMILARITY.
DISULFID	412	438	BY SIMILARITY.
DISULFID	440	449	BY SIMILARITY.
DISULFID	452	462	BY SIMILARITY.
DISULFID	465	478	BY SIMILARITY.
DISULFID	467	482	BY SIMILARITY.
DISULFID	484	493	BY SIMILARITY.
DISULFID	496	511	BY SIMILARITY.
DISULFID	753	762	BY SIMILARITY.
DISULFID	755	769	BY SIMILARITY.
DISULFID	772	781	BY SIMILARITY.
DISULFID	784	800	BY SIMILARITY.
DISULFID	803	818	BY SIMILARITY.
DISULFID	805	828	BY SIMILARITY.
DISULFID	831	840	BY SIMILARITY.
DISULFID	843	858	BY SIMILARITY.
DISULFID	861	875	BY SIMILARITY.
DISULFID	863	882	BY SIMILARITY.
DISULFID	885	894	BY SIMILARITY.
DISULFID	897	911	BY SIMILARITY.
DISULFID	914	926	BY SIMILARITY.
DISULFID	916	933	BY SIMILARITY.
DISULFID	935	944	BY SIMILARITY.
DISULFID	947	960	BY SIMILARITY.
DISULFID	963	975	BY SIMILARITY.
DISULFID	965	981	BY SIMILARITY.
FT	983	992	BY SIMILARITY.
FT	995	1007	BY SIMILARITY.
FT	1010	1019	BY SIMILARITY.
FT	1012	1026	BY SIMILARITY.
FT	1028	1037	BY SIMILARITY.
FT	1040	1053	BY SIMILARITY.
FT	1056	1068	BY SIMILARITY.
FT	1058	1075	BY SIMILARITY.
FT	1077	1086	BY SIMILARITY.
FT	1089	1099	BY SIMILARITY.
FT	1416	1425	BY SIMILARITY.
FT	1432	1432	BY SIMILARITY.

FT	DISULFID	1435	1444	BY SIMILARITY.
FT	DISULFID	1447	1462	BY SIMILARITY.
FT	DISULFID	1465	1480	BY SIMILARITY.
FT	DISULFID	1467	1490	BY SIMILARITY.
FT	DISULFID	1493	1502	BY SIMILARITY.
FT	DISULFID	1505	1520	BY SIMILARITY.
FT	DISULFID	1523	1535	BY SIMILARITY.
FT	DISULFID	1525	1542	BY SIMILARITY.
FT	DISULFID	1544	1553	BY SIMILARITY.
FT	DISULFID	1556	1567	BY SIMILARITY.
FT	DISULFID	1570	1570	INTERCHAIN (PROBABLE).
FT	DISULFID	1574	1574	INTERCHAIN (PROBABLE).
FT	CARBOHYD	51	51	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	85	85	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	299	299	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	359	359	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	376	376	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	466	466	N-LINKED (GLCNAC. . .) (POTENTIAL).
Qy	42 GTCVNCR-	7.6%	Score 178; DB 1; Length 3106;	
Best Local Similarity 20.7%; Fred. No. 0.0013;	Matches 100; Conservative 39; Mismatches 147; Indels 196; Gaps 26;			
Db	767 GECLNKKDHHTGGPYCNELCPSFY--GDPTRGSPEDCQPCAPLNIPNSNFSPTCHLDLR-	87		
Qy	88 SVTNAGDLATLATOCTQSTQCPGTAQDGVTDVDRSAQCVKCPENFYNGGSPQGEAPC	147		
Db	823 ---SGLICD-ECPIG-----YTGPRCERAGYF--GQP--SVPG 855			
Qy	148 VQVFAAGAAAAGVAAVTSQCPQCLNKNDSPATAGAQANLATOCSNOCPGTVLDDGVTL 207			
Db	856 -----GSCOPQCQCNNDLSDIPSQCDLSLGSCL-ICRPG----- 888			
Qy	208 VENTSATLVCRPNNFYNGGSPQGEAPGQVFAAGAAAAGVAAVTSQCPQCLNKND-	266		
Db	889 ---TIGRYCELADGYF-----GDAINTKNCQPCRDINGS 922			
Qy	267 -----PATAGAQAN--LATQG-----STQCP 285			
Db	923 SEDCHTRTGQCECRPNVQGRHCDECKPTEFGQLRGCLPCNCNSFGSKSFDECEASGCC-	981		
Qy	286 TGTATODGTVLVSNSSTQCSQ1ANFYFFGNGFEGKSQCLKCPV-----KTTDAH 337			
Db	982 ---WQCPGV-----AGKCRDCRAHGYF-----NFQEG-----GCIACDCSHLGNNCDPKTGGCI 1027			
Qy	338 APGN-TATQATQCL-----TTCPAGTGTDDGTNFVA-----SATDCT 375			
Db	1028 CPPNNTGECSECLPNTWGHISIVGCKVNCNSTGSLAQSCNNTGQCSCHPKFSGMCKS 1087			
Qy	376 KCSAGFF---ASKTGTGAGTD---TCTBCTKTL-----TSGATAKYAAATORVOCAST 424			
Db	1088 ECSRSHWNYPLCTLCDCFLPGTDATCDETRKCSCSDGTQGCSCKVNVGHCDRCPG 1147			
Qy	425 TFP 426			
Db	1148 KF 1149			
RESULT 12				
ID LMG1_MOUSE	STANDARD; PRT; 1607 AA.			
AC P02468;				
DT 21-JUL-1986 (Rel. 01, Created)				
DT 01-JUL-1989 (Rel. 11, Last sequence update)				
DT 15-JUN-2002 (Rel. 41, Last annotation update)				
GN LAMC1 OR LAMC-1 OR LAMB-2.				
OS Mus musculus (Mouse).				
OC Mammalia; Eulacozia; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_TaxID 10090;				



RESULT 13

LMG3\_HUMAN STANDARD; PRT; 1587 AA.

AC Q916N6; FT SIGNAL CHAIN 1 19

AC Q916N6; FT DOMAIN 20 1597

DR 15-JUN-2002 (Rel. 41, Created) FT DOMAIN 20 1597

DR 15-JUN-2002 (Rel. 41, Last sequence update) FT DOMAIN 271 270

DR 15-JUN-2002 (Rel. 41, Last annotation update) FT DOMAIN 327 326

DE Laminin gamma-3 chain precursor (Laminin 12 gamma 3). FT DOMAIN 383 429

GN LAMC3. FT DOMAIN 430 479

OS Homo sapiens (Human). FT DOMAIN 480 489

EU Homo sapiens (Human). FT DOMAIN 490 519

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; FT DOMAIN 673 672

OC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo. FT DOMAIN 707 706

OX NCBI\_TAXID=9606; FT DOMAIN 755 754

RN [1]. FT DOMAIN 810 809

RP SEQUENCE FROM N.A. FT DOMAIN 866 916

RC TISSUE-Placenta; FT DOMAIN 917 916

RC MEDLINE=992261; PubMed=1022590; FT DOMAIN 965 1013

RA Koch M., Olson P.F., Albus A., Jin W., Hunter D.D., Brunkent W.J., FT DOMAIN 1014 1587

RA Burgess R.E., Champiaud M.F.; FT DOMAIN 1071 1141

RT "Characterization and expression of the laminin gamma3 chain: a novel, FT DOMAIN 1200 1229

RT non-basement membrane-associated, laminin chain."; FT DOMAIN 1424 1504

RL J. Cell Biol. 145: 605-618(1999). FT DOMAIN 1535 1579

CC -I- FUNCTION: Binding to cells via a high affinity receptor, laminin FT DOMAIN 1579 1061

CC is thought to mediate the attachment, migration, and organization FT DOMAIN 87 87

CC of cells into tissues during embryonic development by interacting FT DOMAIN 119 119

CC with other extracellular matrix components. FT DOMAIN 295 295

CC -I- SUBUNIT: Laminin is a complex glycoprotein, consisting of three FT DOMAIN 328 328

CC different polypeptide chains (alpha, beta, gamma), which are bound FT DOMAIN 631 631

CC to each other by disulfide bonds into a cross-shaped molecule. FT DOMAIN 837 837

CC Comprising one long and three short arms with globules at each FT DOMAIN 980 980

CC end. FT DOMAIN 1185 1185

CC THE GAMMA-3 CHAIN IS A SUBUNIT OF LAMININ-12. FT DOMAIN 1518 1518

CC -I- SUBCELLULAR LOCATION: Extracellular. SQ SEQUENCE 1587 AA; 172051 MW; 3CB6509B5F20319 CRC64;

CC -I- TISSUE SPECIFICITY: Broadly expressed in: skin, heart, lung, and FT DOMAIN 175 175

CC the reproductive tracts. Score 7.5%;

CC -I- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT Best Local Similarity 19.7%; Pred. No. 0.00011;

CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE. Matches 89; Conservative 43; Mismatches 155; Indels 164; Gaps 21;

CC -I- DOMAIN: DOMAIN IV IS GLOBULAR. FT DOMAIN 649 649

CC -I- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI). FT DOMAIN 692 AS-----CVPCTCNOHTC----DPNTGICVCSIHTEGES-----702

CC -I- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV. FT DOMAIN 69 69

CC This SWISS-PROT entry is copyright. It is produced through a collaboration FT DOMAIN 127 127

CC between the Swiss Institute of Bioinformatics and the EMBL outstation - CICKKPNFVYNGSP-----TQCPTGTAUDGVTDFDRSAAQ 126

CC the European Bioinformatics Institute. There are no restrictions on its FT DOMAIN 733 733

CC use by non-profit institutions as long as its content is in no way FT DOMAIN 158 158

CC modified and this statement is not removed. Usage by and for commercial FT DOMAIN 733 CERPLGFF----GNPFAQQADDQCPCPGQSACTTIPESGEVVCTHCPPGQRGRCEVYC 789

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch). FT DOMAIN 159 159

DR P041835; Aad36991.1; - FT DOMAIN 790 790

DR HSSP; P02468; 1LE. FT DOMAIN 836

DR Genew; HGNC:6194; LAMC3.

DR MIM: 604349; -

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR001886; LamMT.

DR InterPro; IPR000034; Laminin\_B.

DR Pfam; PF00052; laminin\_B; 1.

DR Pfam; PF00053; laminin\_EGF; 10.

DR Pfam; PF00055; laminin\_Nterm; 1.

DR PRNTS; PR0001; EGFLAMININ.

DR ProDom; PD000082; Lammy; 1.

DR ProDom; PD00031; Laminin\_1; 1.

DR SMART; SM00180; EGF\_Lam; 10.

DR SMART; SM00001; EGF\_like; 1.

DR SMART; SM00281; LamB; 1.

DR SMART; SM00136; LamNT; 1.

DR PROSITE; PS00022; EGF\_1; 7.

DR PROSITE; PS01186; EGF\_2; 2.

DR PROSITE; PS01248; LAMININ\_TYPE-EGF; 10.

KW Glycoprotein; Basement membrane; Extracellular matrix; Cell adhesion; Repeat; Signal; Coiled coil;

KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.

AC	P11046; Q26328; Q9XZT4; Q9VLW6;	CC	to each other by disulfide bonds into a cross-shaped molecule
DT	01-JUL-1989 (Rel. 11, Created)	CC	Comprising one long and three short arms with globules at each
DT	16-OCT-2001 (Rel. 40, Last sequence update)	CC	end.
DT	15-JUN-2002 (Rel. 41, Last annotation update)	CC	SUBCELLULAR LOCATION: Extracellular.
DE	Laminin beta-1 chain precursor (laminin B1 chain).	CC	-1 - TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
GN	LAMB1 OR LAMB1 OR CG1123	CC	COMPONENT).
OS	Drosophila melanogaster (Fruit fly)	CC	-1 - DOMAIN: THE ALPHA HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
OC	Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;	CC	WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
OC	Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;	CC	-1 - DOMAIN: DOMAINS V AND IV ARE GLOBULAR.
OC	Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.	CC	-1 - SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
OX	NCB1:Taxid=7227;	CC	-1 - SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.
RN	[1]	CC	-1 - SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.
RP	SEQUENCE FROM N.A.	CC	-----
RC	STRAIN=Cancan-S;	CC	SEQUENCE FROM N.A.
RX	Medline=88210471; PubMed=3365769;	CC	-----
RX	Medline=94000382; PubMed=3397815;	CC	SEQUENCE FROM N.A.
RA	Gow C.-H., Chang H.-Y., Lih C.-J., Chang T.-W., Hui C.-F.;	CC	-----
RA	"Drosophila substrate adhesion molecule: sequence of laminin B1 chain	CC	SEQUENCE FROM N.A.
RT	"Analysis of the Drosophila gene for the laminin B1 chain."	CC	-----
RT	reveals domains of homology with mouse."	CC	SEQUENCE FROM N.A.
RL	RNA Cell Biol. 12: 573-587(1993).	CC	-----
RN	[2]	CC	-----
RP	SEQUENCE FROM N.A.	CC	-----
RC	STRAIN=Berkeley;	CC	SEQUENCE FROM N.A.
RX	Medline=20156006; PubMed=10713132;	CC	-----
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,	CC	SEQUENCE FROM N.A.
RA	Ananatides P.G., Scheerer S.E., Li P.W., Hoskins R.A., Galle R.F.,	CC	-----
RA	George R.A., Worthman J.R., Yandell M.D., Zhang Q., Chen L.X.,	CC	SEQUENCE FROM N.A.
RA	Sutton G.G., Wortman J.R., Yandell M.D., Champé M., Beiffier B.D.,	CC	-----
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champé M., Beiffier B.D.,	CC	SEQUENCE FROM N.A.
RA	Wan K.H., Doyle C., Baxter G., Nelson C.R., Miklos G.I.G.,	CC	-----
RA	Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,	CC	SEQUENCE FROM N.A.
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,	CC	-----
RA	Beezon K.Y., Benos P.V., Berman B.P., Bolshakov S.,	CC	SEQUENCE FROM N.A.
RA	Borkova D., Botchan M.R., Bokstein P., Brotkier P.,	CC	-----
RA	Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,	CC	SEQUENCE FROM N.A.
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,	CC	-----
RA	de Pablos B., Delcher A., Deng Z., Dey A.D., Dew I., Dietz S.M.,	CC	SEQUENCE FROM N.A.
RA	Dodson K., Doup L.E., Downes M., Duran-Rocha S., Dunkov B.C., Dunn P.,	CC	-----
RA	Durbin R.K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,	CC	SEQUENCE FROM N.A.
RA	Fosler C., Gabrilian A.E., Garg N.S., Gelbart W.M., Glasser K.,	CC	-----
RA	Gloeo A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,	CC	SEQUENCE FROM N.A.
RA	Hoeck N.L., Harvey D., Hernandez J.R., Houck J.,	CC	-----
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ikegami C.,	CC	SEQUENCE FROM N.A.
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennard J.A., Ketchum K.A.,	CC	-----
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,	CC	SEQUENCE FROM N.A.
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,	CC	-----
RA	Liu X., Mattei B., McInnis M.P., McPherson D.,	CC	SEQUENCE FROM N.A.
RA	Merkulov G., Milshina N.V., Mobarrey C., Morris J., Moskrafi A.,	CC	-----
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,	CC	SEQUENCE FROM N.A.
RA	Nelson D.R., Nelson K.A., Nixon D.R., Pacieb J.M.,	CC	-----
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J.J., Puri V., Reese M.G.,	CC	SEQUENCE FROM N.A.
RA	Reinert K., Renington K., Saunders R.D.C., Scheeler F., Shen H.,	CC	-----
RA	Shue B.C., Sien-Klamo I., Skupski M.P., Smith T.,	CC	SEQUENCE FROM N.A.
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,	CC	-----
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,	CC	SEQUENCE FROM N.A.
RA	Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach H.J.,	CC	-----
RA	Williams S.M., Woodward T., Worley K.C., Wu D., Yang S., Yao Q.A.,	CC	SEQUENCE FROM N.A.
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,	CC	-----
RA	Zheng X.H., Zhong F.N., Zhou X., Zhu X., Smith H.O.,	CC	SEQUENCE FROM N.A.
RA	Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.,	CC	-----
RT	"The genome sequence of Drosophila melanogaster."	CC	-----
RL	Science 287:2185-2195 (2000).	CC	-----
CC	-!- FUNCTION: Binding to cells via a high affinity receptor, laminin	CC	-----
CC	is thought to mediate the attachment, migration, and organization	CC	-----
CC	of cells into tissues during embryonic development by interacting	CC	-----
CC	with other extracellular matrix components.	CC	-----
CC	-!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three	CC	-----
CC	different polypeptide chains (alpha, beta, gamma), which are bound	CC	-----

FT	DISULFID	399	417	BY SIMILARITY.	Qy	245	AAAGVAAVTSQCVPQCINKNDSPATAGAQANLATOCSSTOCPIGTAI0DGVTILVFSN----	300
FT	DISULFID	420	433	BY SIMILARITY.	Db	932	----- -CRPC-----	
FT	DISULFID	422	448	BY SIMILARITY.	Qy	301	----- SSTOC5Q1ANYFFNGNFEAGKSQCLKCPYSKTPAHA5GNTAQATQCL----	350
FT	DISULFID	450	459	BY SIMILARITY.	Db	962	CHCQE5G5S5RCETCA5DFF--GNP5D-GT5SKC5NNYDLYDGTGNC5D5RGTGACLKCL	1018
FT	DISULFID	462	477	BY SIMILARITY.	Qy	351	-TTCAGT5VLDGT5TNF5V5A5T- CTKCSAGFF5ASKTT----GFT-----	390
FT	DISULFID	480	493	BY SIMILARITY.	Db	1019	YQFTG5H5C5L5CKD5----FFGDALQNC5Q5C5C5DF5LTG5NTIA5HCD5RTGGC5C5L5PNVQG	1074
FT	DISULFID	482	500	BY SIMILARITY.	Qy	391	AG5DT5C5T5K5L5G5T5G5T5A5K5Y5A5T5VQ5C	421
FT	DISULFID	502	511	BY SIMILARITY.	Db	1075	VRCDQ5C5A5N5H5K5T5G5-----EG5C5C5NC	1098
FT	DISULFID	514	528	BY SIMILARITY.				
FT	DISULFID	791	803	BY SIMILARITY.				
FT	DISULFID	793	810	BY SIMILARITY.				
FT	DISULFID	812	821	BY SIMILARITY.				
FT	DISULFID	824	836	BY SIMILARITY.				
FT	DISULFID	839	851	BY SIMILARITY.				
FT	DISULFID	841	858	BY SIMILARITY.				
FT	DISULFID	860	869	BY SIMILARITY.				
FT	DISULFID	872	882	BY SIMILARITY.				
FT	DISULFID	885	894	BY SIMILARITY.				
FT	DISULFID	887	901	BY SIMILARITY.				
FT	DISULFID	904	913	BY SIMILARITY.				
FT	DISULFID	916	932	BY SIMILARITY.				
FT	DISULFID	935	951	BY SIMILARITY.				
FT	DISULFID	937	962	BY SIMILARITY.				
FT	DISULFID	964	973	BY SIMILARITY.				
FT	DISULFID	976	990	BY SIMILARITY.				
FT	DISULFID	993	1007	BY SIMILARITY.				
FT	DISULFID	995	1014	BY SIMILARITY.				
FT	DISULFID	1017	1026	BY SIMILARITY.				
FT	DISULFID	1029	1042	BY SIMILARITY.				
FT	DISULFID	1045	1059	BY SIMILARITY.				
FT	DISULFID	1047	1066	BY SIMILARITY.				
FT	DISULFID	1068	1077	BY SIMILARITY.				
FT	DISULFID	1080	1093	BY SIMILARITY.				
FT	DISULFID	1096	1108	BY SIMILARITY.				
FT	DISULFID	1098	1115	BY SIMILARITY.				
FT	DISULFID	1117	1126	BY SIMILARITY.				
FT	DISULFID	1123	1141	BY SIMILARITY.				
FT	DISULFID	1144	1156	BY SIMILARITY.				
FT	DISULFID	1146	1163	BY SIMILARITY.				
FT	DISULFID	1165	1174	BY SIMILARITY.				
FT	DISULFID	1177	1188	BY SIMILARITY.				
FT	DISULFID	1191	1191	INTERCHAIN (PROBABLE).				
FT	DISULFID	1194	1194	INTERCHAIN (PROBABLE).				
FT	DISULFID	1788	1788	INTERCHAIN (PROBABLE).				
FT	SITE	643	645	CELL ATTACHMENT SITE (POTENTIAL).				
FT	CAROHYD	140	140	N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CAROHYD	203	203	N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CAROHYD	234	234	N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CAROHYD	489	489	N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CAROHYD	593	593	N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CAROHYD	1053	1053	N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CAROHYD	1248	1248	N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CAROHYD	1303	1303	N-LINKED (GLCNAC. . .) (POTENTIAL).				
Query Match		7.4%	Score 173;	DB: 1; Length 1790;				
Best Local Similarity	21.5%	Pred: No. 0.00017;	Matches 97; Conservative 37; Mismatches 14;	Indels 170; Gaps 23;				
Qy	10	IISLFINFLRAYPC	---PDGTQTOAGLTDYGAADL5TCVNCRPNFYNGGAAQGEANGNQ	66				
Db	779	IISVFVHB-GASMNCNCPNTG	---LSKVCESNGYC-QCKPNTV-GRQCDQCAPGT	829				
Qy	67	PFANNAARGICVPCQ1N	RGVSYTNAGDLAYLATQ5TQCPTGTAI0DDGTDFDRSAQ	126				
Db	830	GFPPEG	---CKACDCNSIGSKDKYCDLITG5QCQC-----VPNTYGR-E	868				
Qy	127	CVKCPNFIYNGGSPQCBAPGVQFVAGAAQGEANGNQ	66					
Db	869	CNCQCPYW	---NPFBCRVCQCN5HATCDP1QGC5C5DCQ---DS-----	907				
Qy	187	LATQCSNQCPGTVLDGVTLVENTSATLVCYKCRPNFYNG-	-GSFQGEAPGVQVFARGA	244				
Db	908		-----TRG5CDSDCL5Y5G5NPL5FG5EIG-----	931				

RESULT 15  
LMG3\_MOUSE  
ID LMG3\_MOUSE STANDARD: ERT: 1581 AA.  
AC Q9RQB6; Q9W7W6;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Laminin gamma-3 chain precursor (Laminin 12 gamma 3).  
GN LAMC3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OC NCBI\_TaxID=10090;  
RN [1]  
RN SEQUENCE FROM N.A.  
RA Albus A.M.; Burgeson B.; Champiliaud M.-F.; Koch M.; Olson P.;  
RT "Mouse laminin 12 gamma 3 chain."  
RL Submitted (AUG-1998) to the EMBL/GenBank/DDJB databases.  
RN [2]  
RN SEQUENCE OF 1-1526 FROM N.A.  
RX MEDLINE=9953969; PubMed=10318827;  
RA Iivanainen A.; Morita T.; Trygvason K.;  
RT Molecular cloning and tissue specific expression of a novel murine  
RT laminin gamma3 chain;  
RL J. Biol. Chem. 274:14107-14111(1999).  
CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin  
CC is thought to mediate the attachment, migration, and organization  
CC of cells into tissues during embryonic development by interacting  
CC with other extracellular matrix components.  
CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three  
CC different polypeptide chains (alpha, beta, gamma), which are bound  
CC to each other by disulfide bonds into a cross-shaped molecule  
CC comprising one long and three short arms with globules at each  
CC end.  
CC -1- THE GAMMA-3 CHAIN IS A SUBUNIT OF LAMININ-12.  
CC -1- SUBCELLULAR LOCATION: Extracellular.  
CC -1- TISSUE SPECIFICITY: Strongly expressed in capillaries and  
arteries of kidney as well as in interstitial Leydig cells of  
testis.  
CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT  
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.  
CC -1- DOMAIN: DOMAIN IV IS GLOBULAR.  
CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).  
CC -1- SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAINS.  
CC -1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.  
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or send an email to license@ebi.ac.uk).  
DR EMBL; AF083372; AF08983; 1; -

